Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-17. (Canceled)

18. (Original) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*;

collecting the sample from the environment;

extracting the sample's DNA;

obtaining DNA standards from a culture of *Stachybotrys chartarum*;

determining the concentration of *Stachybotrys chartarum* spores in the DNA standards;

amplifying by polymerase chain reaction each of the DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the DNA standards and the collected sample's DNA to obtain an indication of the presence of the fungus *Stachybotrys chartarum* in the collected sample and a concentration of the fungus *Stachybotrys chartarum* in the collected sample.

19. (Currently amended) The method of claim 18, wherein the primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 1) 5'GTTGCTTCGGCGGGAAC3';

a reverse primer comprising a base sequence (SEQ ID NO: 2) 5'TTTGCGTTTGCCACTCAGAG3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA, wherein the forward primer, reverse primer and probe do not cross-react with other fungal species when used in combination in polymerase chain reaction.

20. (Currently amended) The method of claim 18, wherein the primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 3) 5'ACCTATCGTTGCTTCGGCG3';

a reverse primer comprising a base sequence (SEQ ID NO: 4) 5'GCGTTTGCCACTCAGAGAATACT3'; and

a probe comprising a base sequence (SEQ ID NO 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA, wherein the forward primer, reverse primer and probe do not cross-react with other fungal species when used in combination in polymerase chain reaction.

21. (Previously presented) The method of claim 18, wherein the concentration of *Stachybotrys chartarum* spores in the DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.

22. (Currently amended) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*,

wherein the obtained primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 1) 5'GTTGCTTCGGCGGGAAC3';

a reverse primer comprising a base sequence (SEQ ID NO: 2) 5'TTTGCGTTTGCCACTCAGAG3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA; and

employing quantitative polymerase chain reaction, using the obtained primer and probe set, to determine a concentration of the fungus *Stachybotrys chartarum* in the collected sample, wherein the forward primer, reverse primer and probe do not cross-react with other fungal species when used in combination in the quantitative polymerase chain reaction.

23. (Previously presented) The method of claim 22, wherein employing quantitative polymerase chain reaction further comprises:

extracting the collected sample's DNA;

obtaining one or more DNA standards from a culture of *Stachybotrys chartarum*;

determining a concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards;

amplifying by polymerase chain reaction each of the one or more DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the one or more DNA standards and the collected sample's DNA to determine the concentration of the fungus *Stachybotrys chartarum* in the collected sample.

24. (Previously presented) The method of claim 23, wherein the concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.

25. (Currently amended) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*,

wherein the obtained primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 3)

5'ACCTATCGTTGCTTCGGCG3';

a reverse primer comprising a base sequence (SEQ ID NO: 4) 5'GCGTTTGCCACTCAGAGAATACT3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAM; and

employing quantitative polymerase chain reaction, using the obtained primer and probe set, to determine a concentration of the fungus *Stachybotrys chartarum* in the collected sample, wherein the forward primer, reverse primer and probe do not cross-react with other fungal species when used in combination in the quantitative polymerase chain reaction.

26. (Previously presented) The method of claim 25, wherein employing quantitative polymerase chain reaction further comprises:

extracting the collected sample's DNA;

obtaining one or more DNA standards from a culture of *Stachybotrys chartarum*;

determining a concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards;

amplifying by polymerase chain reaction each of the one or more DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the one or more DNA standards and the collected sample's DNA to determine the concentration of the fungus *Stachybotrys chartarum* in the collected sample.

27. (Previously presented) The method of claim 26, wherein the concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.